

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/674,817

DATE: 05/08/2001  
TIME: 11:50:03

Input Set : A:\ES.txt  
Output Set: N:\CRF3\05082001\I674817.raw

**ENTERED**

3 <110> APPLICANT: Lorz, et al.  
5 <120> TITLE OF INVENTION: NUCLEIC ACID MOLECULES WHICH CODE FOR ENZYMES DERIVED FROM WHEAT AND  
6 WHICH ARE INVOLVED IN THE SYNTHESIS OF STARCH  
8 <130> FILE REFERENCE: 514413-3849  
10 <140> CURRENT APPLICATION NUMBER: 09/674,817  
C--> 11 <141> CURRENT FILING DATE: 2001-04-06  
13 <150> PRIOR APPLICATION NUMBER: PCT/EP99/03141  
14 <151> PRIOR FILING DATE: 1999-05-07  
16 <150> PRIOR APPLICATION NUMBER: 19820608.9  
17 <151> PRIOR FILING DATE: 1998-05-08  
19 <160> NUMBER OF SEQ ID NOS: 10  
21 <170> SOFTWARE: PatentIn version 3.0  
23 <210> SEQ ID NO: 1  
24 <211> LENGTH: 2997  
25 <212> TYPE: DNA  
26 <213> ORGANISM: Triticum aestivum L. cv. Florida  
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29 <221> NAME/KEY: CDS  
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31 <223> OTHER INFORMATION: exon 1  
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36 <222> LOCATION: (2145)..(2921)  
37 <223> OTHER INFORMATION: exon 3  
40 <220> FEATURE:  
41 <221> NAME/KEY: Intron  
42 <222> LOCATION: (297)..(396)  
43 <223> OTHER INFORMATION: intron 1  
46 <220> FEATURE:  
47 <221> NAME/KEY: CDS  
48 <222> LOCATION: (397)..(1617)  
49 <223> OTHER INFORMATION: exon 2  
52 <220> FEATURE:  
53 <221> NAME/KEY: Intron  
54 <222> LOCATION: (1618)..(2144)  
55 <223> OTHER INFORMATION: intron 2  
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59 gg tcg ggg ccg gcg ccg cgc ctg cga cgg tgg cga ccc aat gcg acg 47  
60 Ser Gly Pro Ala Pro Arg Leu Arg Arg Trp Arg Pro Asn Ala Thr  
61 1 5 10 15  
63 gcg ggg aag ggg gtc ggc gag gtg tgc gcc gcg gtt gtc gag gcg gcg 95  
64 Ala Gly Lys Gly Val Gly Glu Val Cys Ala Ala Val Val Glu Ala Ala  
65 20 25 30  
67 acg aag gta gag gac gag ggg gag gag gac gag ccg gtg gcg gag gac 143  
68 Thr Lys Val Glu Asp Glu Gly Glu Glu Asp Glu Pro Val Ala Glu Asp  
69 35 40 45  
71 agg tac gcg ctc ggc ggc gcg tgc agg gtg ctc gcc gga atg ccc gcg 191

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72 Arg Tyr Ala Leu Gly Gly Ala Cys Arg Val Leu Ala Gly Met Pro Ala
73      50      55      60
75 ccg ctg ggc gcc acc gcg ctc gcc ggc ggg gtc aat ttc gcc gtc tat      239
76 Pro Leu Gly Ala Thr Ala Leu Ala Gly Gly Val Asn Phe Ala Val Tyr
77      65      70      75
79 tcc ggc gga gcc acc gcc gcg gcg ctc tgc ctc ttc acg cca gaa gat      287
80 Ser Gly Gly Ala Thr Ala Ala Ala Leu Cys Leu Phe Thr Pro Glu Asp
81 80      85      90      95
83 ctc aag gcg gtgggggttgc ctcccgagta gagttcatca gctttgcgtg      336
84 Leu Lys Ala
87 cgccgcgcgc cccttttttg ggcctgcaat ttaagttttg tactggggca aatgctgcag      396
89 gat agg gtg acc gag gag gtt ccc ctt gac ccc ctg atg aat cgg acc      444
90 Asp Arg Val Thr Glu Glu Val Pro Leu Asp Pro Leu Met Asn Arg Thr
91      100      105      110
93 ggg aac gtg tgg cat gtc ttc atc gaa ggc gag ctg cac aac atg ctt      492
94 Gly Asn Val Trp His Val Phe Ile Glu Gly Glu Leu His Asn Met Leu
95 115      120      125      130
97 tac ggg tac agg ttc gac ggc acc ttt gct cct cac tgc ggg cac tac      540
98 Tyr Gly Tyr Arg Phe Asp Gly Thr Phe Ala Pro His Cys Gly His Tyr
99      135      140      145
101 ctt gat gtt tcc aat gtc gtg gtg gat cct tat gct aag gca gtg ata      588
102 Leu Asp Val Ser Asn Val Val Val Asp Pro Tyr Ala Lys Ala Val Ile
103      150      155      160
105 agc cga ggg gag tat ggt gtt cca gcg cgt ggt aac aat tgc tgg cct      636
106 Ser Arg Gly Glu Tyr Gly Val Pro Ala Arg Gly Asn Asn Cys Trp Pro
107      165      170      175
109 cag atg gct ggc atg atc cct ctt cca tat agc acg ttt gat tgg gaa      684
110 Gln Met Ala Gly Met Ile Pro Leu Pro Tyr Ser Thr Phe Asp Trp Glu
111      180      185      190
113 ggc gac cta cct cta aga tat cct caa aag gac ctg gta ata tat gag      732
114 Gly Asp Leu Pro Leu Arg Tyr Pro Gln Lys Asp Leu Val Ile Tyr Glu
115 195      200      205      210
117 atg cac ttg cgt gga ttc acg aag cat gat tca agc aat gta gaa cat      780
118 Met His Leu Arg Gly Phe Thr Lys His Asp Ser Ser Asn Val Glu His
119      215      220      225
121 ccg ggt act ttc att gga gct gtg tgc aag ctt gac tat ttg aag gag      828
122 Pro Gly Thr Phe Ile Gly Ala Val Ser Lys Leu Asp Tyr Leu Lys Glu
123      230      235      240
125 ctt gga gtt aat tgt att gaa tta atg ccc tgc cat gag ttc aac gag      876
126 Leu Gly Val Asn Cys Ile Glu Leu Met Pro Cys His Glu Phe Asn Glu
127      245      250      255
129 ctg gag tac tca acc tct tct tcc aag atg aac ttt tgg gga tat tct      924
130 Leu Glu Tyr Ser Thr Ser Ser Ser Lys Met Asn Phe Trp Gly Tyr Ser
131      260      265      270
133 acc ata aac ttc ttt tca cca atg aca aga tac aca tca ggc ggg ata      972
134 Thr Ile Asn Phe Phe Ser Pro Met Thr Arg Tyr Thr Ser Gly Gly Ile
135 275      280      285      290
137 aaa aac tgt ggg cgt gat gcc ata aat gag ttc aaa act ttt gta aga      1020
138 Lys Asn Cys Gly Arg Asp Ala Ile Asn Glu Phe Lys Thr Phe Val Arg

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139		295		300		305		
141	gag gct cac	aaa cgg gga att	gag gtg atc ctg gat gtt	gtc ttc aac		1068		
142	Glu Ala His	Lys Arg Gly Ile	Glu Val Ile Leu Asp Val	Val Phe Asn				
143		310		315		320		
145	cat aca gct	gag ggt aat gag aat	ggt cca ata tta tca	ttt aag ggg		1116		
146	His Thr Ala	Glu Gly Asn Glu Asn	Gly Pro Ile Leu Ser	Phe Lys Gly				
147		325		330		335		
149	gtc gat aat	act aca tac tat atg	ctt gca ccc aag gga	gag ttt tat		1164		
150	Val Asp Asn	Thr Thr Tyr Tyr Met	Leu Ala Pro Lys Gly	Glu Phe Tyr				
151		340		345		350		
153	aac tat tct	ggc tgt ggg aat acc	ttc aac tgt aat cat	cct gtg gtt		1212		
154	Asn Tyr Ser	Gly Cys Gly Asn Thr	Phe Asn Cys Asn His	Pro Val Val				
155	355		360		365		370	
157	cgt caa ttc	att gta gat tgt tta	aga tac tgg gtg acg	gaa atg cat		1260		
158	Arg Gln Phe	Ile Val Asp Cys Leu	Arg Tyr Trp Val Thr	Glu Met His				
159		375		380		385		
161	gtt gat ggt	ttt cgt ttt gat ctt	gca tcc ata atg acc	aga ggt tcc		1308		
162	Val Asp Gly	Phe Arg Phe Asp Leu	Ala Ser Ile Met Thr	Arg Gly Ser				
163		390		395		400		
165	agt ctg tgg	gat cca gtt aac gtg	tat gga gct cca ata	gaa ggt gac		1356		
166	Ser Leu Trp	Asp Pro Val Asn Val	Tyr Gly Ala Pro Ile	Glu Gly Asp				
167		405		410		415		
169	atg atc aca	aca ggg aca cct ctt	ggt act cca cca ctt	att gac atg		1404		
170	Met Ile Thr	Thr Gly Thr Pro Leu	Val Thr Pro Pro Leu	Ile Asp Met				
171		420		425		430		
173	atc agc aat	gac cca att ctt gga	ggc gtc aag ctc att	gct gaa gca		1452		
174	Ile Ser Asn	Asp Pro Ile Leu Gly	Gly Val Lys Leu Ile	Ala Glu Ala				
175	435		440		445		450	
177	tgg gat gca	gga ggc ctc tat caa	gta ggt caa ttc cct	cac tgg aat		1500		
178	Trp Asp Ala	Gly Gly Leu Tyr Gln	Val Gly Gln Phe Pro	His Trp Asn				
179		455		460		465		
181	gtt tgg tct	gag tgg aat ggg aag	tac cgg gac att gtg	cgt caa ttc		1548		
182	Val Trp Ser	Glu Trp Asn Gly Lys	Tyr Arg Asp Ile Val	Arg Gln Phe				
183		470		475		480		
185	att aaa ggc	act gat gga ttt gct	ggt ggt ttt gcc gaa	tgt ctt tgt		1596		
186	Ile Lys Gly	Thr Asp Gly Phe Ala	Gly Gly Phe Ala Glu	Cys Leu Cys				
187		485		490		495		
189	gga agt cca	cac cta tac cag gta	agttgtg gcaatacttg	taaataagatt		1647		
190	Gly Ser Pro	His Leu Tyr Gln						
191		500		505				
193	gagtgaatgt	cacctggatt ttttatatat	accacatgat gatacacatc	taaataatata		1707		
195	acaatcatag	tgtatgcata tgcatctggc	taagaagtat tagtgtatac	actagtgcata		1767		
197	tatatagggt	ttaacacca acttgccaat	gaaggaacat agggctttct	agttatctta		1827		
199	tttattttgtc	cggtgaataa tccactgaaa	aattccagcc atgtcatttt	ttaggggggg		1887		
201	agaagaaact	atattgatatt gccccctaa	aagaagccat ctcagaattc	ataggtaagt		1947		
203	tgcttttctg	taaagaaagg aaaacgactt	catactttct atcgggtgcta	acttagctcg		2007		
205	atgtatatatt	gtaagatgaa tgccaaattt	aattttgtcgg ataatttgat	ctgttattca		2067		
207	caaattttcta	tttggtttct ctagaaatca	aaccagtaac ttgttatttg	cactgcaact		2127		
209	tcttattgat	taatcag gca gga gga	agg aaa cct tgg cac	agt atc aac		2177		

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	Ala	Gly	Gly	Arg	Lys	Pro	Trp	His	Ser	Ile	Asn						
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211					510					515							
213	ttt	gta	tgt	gca	cat	gat	gga	ttt	aca	ctg	gct	gat	ttg	gta	aca	tat	2225
214	Phe	Val	Cys	Ala	His	Asp	Gly	Phe	Thr	Leu	Ala	Asp	Leu	Val	Thr	Tyr	
215				520					525				530				
217	aat	aag	aag	tac	aat	tta	cca	aat	ggg	gag	aac	aac	aga	gat	gga	gaa	2273
218	Asn	Lys	Lys	Tyr	Asn	Leu	Pro	Asn	Gly	Glu	Asn	Asn	Arg	Asp	Gly	Glu	
219			535					540				545					
221	aat	cac	aat	ctt	agc	tgg	aat	tgt	ggg	gag	gaa	gga	gaa	ttc	gca	aga	2321
222	Asn	His	Asn	Leu	Ser	Trp	Asn	Cys	Gly	Glu	Glu	Gly	Glu	Phe	Ala	Arg	
223		550					555				560						
225	ttg	tct	gtc	aaa	aga	ttg	agg	aag	agg	cag	atg	cgc	aat	ttc	ttt	gtt	2369
226	Leu	Ser	Val	Lys	Arg	Leu	Arg	Lys	Arg	Gln	Met	Arg	Asn	Phe	Phe	Val	
227	565				570					575					580		
229	tgt	ctc	atg	gtt	tct	caa	gga	gtt	cca	atg	ttc	tac	atg	ggg	gat	gaa	2417
230	Cys	Leu	Met	Val	Ser	Gln	Gly	Val	Pro	Met	Phe	Tyr	Met	Gly	Asp	Glu	
231				585					590				595				
233	tat	ggc	cac	aca	aaa	ggg	ggc	aac	aac	aat	aca	tac	tgc	cat	gat	tct	2465
234	Tyr	Gly	His	Thr	Lys	Gly	Gly	Asn	Asn	Thr	Tyr	Cys	His	Asp	Ser		
235			600					605				610					
237	tat	gtc	aat	tat	ttt	cgc	tgg	gat	aaa	aaa	gaa	caa	tac	tct	gag	ttg	2513
238	Tyr	Val	Asn	Tyr	Phe	Arg	Trp	Asp	Lys	Lys	Glu	Gln	Tyr	Ser	Glu	Leu	
239		615					620				625						
241	cac	cga	ttc	tgc	tgc	ctc	atg	acc	aaa	ttc	cgc	aag	gag	tgc	gag	ggg	2561
242	His	Arg	Phe	Cys	Cys	Leu	Met	Thr	Lys	Phe	Arg	Lys	Glu	Cys	Glu	Gly	
243		630				635				640							
245	ctt	ggc	ctt	gag	gac	ttt	cca	acg	gcc	aaa	cgg	ctg	cag	tgg	cat	ggg	2609
246	Leu	Gly	Leu	Glu	Asp	Phe	Pro	Thr	Ala	Lys	Arg	Leu	Gln	Trp	His	Gly	
247	645				650				655				660				
249	cat	cag	cct	ggg	aag	cct	gat	tgg	tct	gag	aat	agc	cga	ttc	gtt	gcc	2657
250	His	Gln	Pro	Gly	Lys	Pro	Asp	Trp	Ser	Glu	Asn	Ser	Arg	Phe	Val	Ala	
251			665					670				675					
253	ttt	tcc	atg	aaa	gat	gaa	aga	cag	ggc	gag	atc	tat	gtg	gcc	ttc	aac	2705
254	Phe	Ser	Met	Lys	Asp	Glu	Arg	Gln	Gly	Glu	Ile	Tyr	Val	Ala	Phe	Asn	
255			680					685				690					
257	acc	agc	cac	tta	ccg	gcc	gtt	gtt	gag	ctc	cca	gag	cgc	gca	ggg	cgc	2753
258	Thr	Ser	His	Leu	Pro	Ala	Val	Val	Glu	Leu	Pro	Glu	Arg	Ala	Gly	Arg	
259			695				700				705						
261	cgg	tgg	gaa	ccg	gtg	gtg	gac	aca	ggc	aag	cca	gca	cca	tac	gac	ttc	2801
262	Arg	Trp	Glu	Pro	Val	Val	Asp	Thr	Gly	Lys	Pro	Ala	Pro	Tyr	Asp	Phe	
263		710				715			720								
265	ctc	acc	gac	gac	tta	cct	gat	cgc	gct	ctc	acc	ata	cac	cag	ttc	tcg	2849
266	Leu	Thr	Asp	Asp	Leu	Pro	Asp	Arg	Ala	Leu	Thr	Ile	His	Gln	Phe	Ser	
267	725				730				735				740				
269	cat	ttc	ctc	tac	tcc	aac	ctc	tac	ccc	atg	ctc	agc	tac	tca	tcg	gtc	2897
270	His	Phe	Leu	Tyr	Ser	Asn	Leu	Tyr	Pro	Met	Leu	Ser	Tyr	Ser	Ser	Val	
271			745					750				755					
273	atc	cta	gta	ttg	cgc	cct	gat	gtt	tgagagacca	atatatacag	taaataatat						2951
274	Ile	Leu	Val	Leu	Arg	Pro	Asp	Val									

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281 <211> LENGTH: 764
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292          20          25          30
295 Lys Val Glu Asp Glu Gly Glu Glu Asp Glu Pro Val Ala Glu Asp Arg
296          35          40          45
299 Tyr Ala Leu Gly Gly Ala Cys Arg Val Leu Ala Gly Met Pro Ala Pro
300          50          55          60
303 Leu Gly Ala Thr Ala Leu Ala Gly Gly Val Asn Phe Ala Val Tyr Ser
304 65          70          75          80
307 Gly Gly Ala Thr Ala Ala Ala Leu Cys Leu Phe Thr Pro Glu Asp Leu
308          85          90          95
311 Lys Ala Asp Arg Val Thr Glu Glu Val Pro Leu Asp Pro Leu Met Asn
312          100         105         110
315 Arg Thr Gly Asn Val Trp His Val Phe Ile Glu Gly Glu Leu His Asn
316          115         120         125
319 Met Leu Tyr Gly Tyr Arg Phe Asp Gly Thr Phe Ala Pro His Cys Gly
320          130         135         140
323 His Tyr Leu Asp Val Ser Asn Val Val Val Asp Pro Tyr Ala Lys Ala
324 145         150         155         160
327 Val Ile Ser Arg Gly Glu Tyr Gly Val Pro Ala Arg Gly Asn Asn Cys
328          165         170         175
331 Trp Pro Gln Met Ala Gly Met Ile Pro Leu Pro Tyr Ser Thr Phe Asp
332          180         185         190
335 Trp Glu Gly Asp Leu Pro Leu Arg Tyr Pro Gln Lys Asp Leu Val Ile
336          195         200         205
339 Tyr Glu Met His Leu Arg Gly Phe Thr Lys His Asp Ser Ser Asn Val
340          210         215         220
343 Glu His Pro Gly Thr Phe Ile Gly Ala Val Ser Lys Leu Asp Tyr Leu
344 225         230         235         240
347 Lys Glu Leu Gly Val Asn Cys Ile Glu Leu Met Pro Cys His Glu Phe
348          245         250         255
351 Asn Glu Leu Glu Tyr Ser Thr Ser Ser Lys Met Asn Phe Trp Gly
352          260         265         270
355 Tyr Ser Thr Ile Asn Phe Phe Ser Pro Met Thr Arg Tyr Thr Ser Gly
356          275         280         285
359 Gly Ile Lys Asn Cys Gly Arg Asp Ala Ile Asn Glu Phe Lys Thr Phe
360          290         295         300
363 Val Arg Glu Ala His Lys Arg Gly Ile Glu Val Ile Leu Asp Val Val
364 305         310         315         320
367 Phe Asn His Thr Ala Glu Gly Asn Glu Asn Gly Pro Ile Leu Ser Phe
368          325         330         335

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VERIFICATION SUMMARY

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Input Set : A:\ES.txt

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L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date